BLAST Basic Local Alignment Search Tool

- •

Blast 2 sequences

X98077:Saito_X2

Results for: [emb|X98077.1 Hepatitis B virus complete genome, wild type(3215bp) ▼]
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST
results for.

Query ID
    gi|1914699|emb|X98077.1|HBVCGWITY
Description
    Hepatitis B virus complete genome, wild type
Molecule type
    nucleic acid
Query Length
    3215

Subject ID
    14321
Description
    None
Molecule type
    nucleic acid
Subject Length
    22
Program
    BLASTN 2.2.20+ Citation

Search Parameters

Program	blastn
Word size	7
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

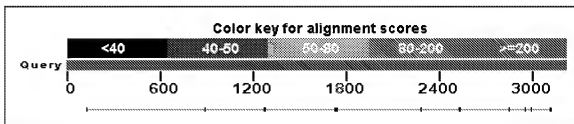| Params	Ungapped	Gapped
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics

Effective search space 38460

Graphic Summary

Distribution of 12 Blast Hits on the Query Sequence

[?]
_____

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

| 0 | 600 | 1200 | 1800 | 2400 | 3000 |

Dot Matrix View

Plot of gi|1914699|emb|X98077.1|HBVCGWITY vs 14321 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: 🗓 UniGene 🗒 GEO 🅖 Gene 🗏 Structure 🗺 Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

14321	26.5	186	2%	4e-04	100%

Alignments **Select All** Get selected sequences Distance tree of results

```
>lcl|14321
Length=22
```

```
 Score = 26.5 bits (28),  Expect = 4e-04
 Identities = 16/17 (94%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query  1728  GAGTGGGAGGAGTTGGG  1744
             || |||||||||||||||
Sbjct  6     GACTGGGAGGAGTTGGG  22


 Score = 17.5 bits (18),  Expect = 0.21
 Identities = 9/9 (100%), Gaps = 0/9 (0%)
 Strand=Plus/Plus

Query  893  GGAGTTGGG  901
            |||||||||
Sbjct  14   GGAGTTGGG  22


 Score = 15.7 bits (16),  Expect = 0.72
 Identities = 8/8 (100%), Gaps = 0/8 (0%)
 Strand=Plus/Plus

Query  1744  GGGAGGAG  1751
             ||||||||
Sbjct  10    GGGAGGAG  17


 Score = 15.7 bits (16),  Expect = 0.72
 Identities = 8/8 (100%), Gaps = 0/8 (0%)
 Strand=Plus/Minus

Query  2282  ACTCCTCC  2289
             ||||||||
Sbjct  18    ACTCCTCC  11


 Score = 13.9 bits (14),  Expect = 2.5
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query  2992  AAGGACT  2998
             |||||||
Sbjct  3     AAGGACT  9


 Score = 13.9 bits (14),  Expect = 2.5
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus

Query  133  GACTGGG  139
            |||||||
Sbjct  6    GACTGGG  12


 Score = 13.9 bits (14),  Expect = 2.5
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Plus
```

```
Query  2849   TGGGAGG   2855
              |||||||
Sbjct  9      TGGGAGG   15
```

```
 Score = 13.9 bits (14),  Expect = 2.5
 Identities = 9/10 (90%), Gaps = 0/10 (0%)
 Strand=Plus/Minus

Query  3116   CAGCTCCTCC   3125
              || |||||||
Sbjct  20     CAACTCCTCC   11
```

```
 Score = 13.9 bits (14),  Expect = 2.5
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query  3122   CTCCTCC   3128
              |||||||
Sbjct  17     CTCCTCC   11
```

```
 Score = 13.9 bits (14),  Expect = 2.5
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query  2531   AACTCCT   2537
              |||||||
Sbjct  19     AACTCCT   13
```

```
 Score = 13.9 bits (14),  Expect = 2.5
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query  1277   AACTCCT   1283
              |||||||
Sbjct  19     AACTCCT   13
```

```
 Score = 13.9 bits (14),  Expect = 2.5
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query  2954   CCAACTC   2960
              |||||||
Sbjct  21     CCAACTC   15
```

Select All Get selected sequences Distance tree of results